

# SCORE Search Results Details for Application 10796719 and Search Result 20070322\_090632\_us-10-796-719a-31.rag.

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GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 23, 2007, 00:36:07 ; Search time 218 Seconds  
(without alignments)  
31.425 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*
- 11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SCORE Search Results Details for Application 10796719 and Search Result 20070322\_090635\_us-10-796-719a-31.rup.

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## OM protein - protein search, using sw model

Run on: March 23, 2007, 00:37:42 ; Search time 346 Seconds  
(without alignments)  
43.381 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4.\*:  
1: uniprot\_sprot:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	93	92.1	61	2	Q6VEG7_ECOLI		Q6veg7 escherichia
2	93	92.1	61	2	Q6VEG8_ECOLI		Q6veg8 escherichia
3	93	92.1	72	1	HST2_ECOLI		Q47185 escherichia

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OM protein - protein search, using sw model

Run on: March 23, 2007, 00:47:23 ; Search time 51 Seconds  
(without alignments)  
24.028 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%
Query	

# SCORE Search Results Details for Application 10796719 and Search Result 20070322\_090649\_us-10-796-719a-31.rapbm.

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GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 23, 2007, 00:48:07 ; Search time 186 Seconds  
(without alignments)  
34.866 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

# SCORE Search Results Details for Application 10796719 and Search Result 20070322\_090655\_us-10-796-719a-31.rapbn.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 00:49:03 ; Search time 90 Seconds  
(without alignments)  
31.666 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

**SCORE Search Results Details for Application  
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### OM protein - protein search, using sw model

Run on: March 23, 2007, 17:56:43 ; Search time 218 Seconds  
(without alignments)  
38.159 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 48933398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_200701:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 17:59:13 ; Search time 344 Seconds  
(without alignments)  
52.983 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_8.4:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	% Match Length DB ID				Description
		1	2	3	4	
1	112	100.0	17	2	Q9R581_VIBCH	Q9r581 vibrio chol
2	112	100.0	18	2	Q9R580_VIBCH	Q9r580 vibrio chol
3	112	100.0	19	2	Q9R579_VIBCH	Q9r579 vibrio chol

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OM protein - protein search, using sw model

Run on: March 23, 2007, 18:02:53 ; Search time 39 Seconds  
(without alignments)  
41.941 Million cell updates/sec

Title: US-10-796-719A-14

Perfect score: 112

Sequence: 1 IDCCEICCNACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	% Match Length DB ID				Description
1	112	100.0	17	2	A54534	heat-stable entero

# SCORE Search Results Details for Application 10796719 and Search Result 20070323\_110730\_us-10-796-719a-14.rai.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 18:09:29 ; Search time 52 Seconds  
(without alignments)  
28.616 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query
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# SCORE Search Results Details for Application 10796719 and Search Result 20070323\_110733\_us-10-796-719a-14.rapbm.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 18:09:38 ; Search time 184 Seconds  
(without alignments)  
42.797 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

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OM protein - protein search, using sw model

Run on: March 23, 2007, 18:10:53 ; Search time 89 Seconds  
(without alignments)  
38.883 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

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## OM protein - protein search, using sw model

Run on: March 26, 2007, 11:50:46 ; Search time 218 Seconds  
(without alignments)  
31.425 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101

Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 48933398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

```
Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SCORE Search Results Details for Application  
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### OM protein - protein search, using sw model

Run on: March 26, 2007, 11:52:20 ; Search time 347 Seconds  
(without alignments)  
43.256 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_8.4.\*  
1: uniprot\_sprot:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8

Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	93	92.1	61	2	Q6VEG7_ECOLI		Q6veg7 escherichia
2	93	92.1	61	2	Q6VEG8_ECOLI		Q6veg8 escherichia
3	93	92.1	72	1	HST2_ECOLI		Q47185 escherichia

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OM protein - protein search, using sw model

Run on: March 26, 2007, 11:56:16 ; Search time 40 Seconds  
(without alignments)  
33.676 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101

Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	%				Description
		Match	Length	DB	ID	
1	93	92.1	72	1	QHEC4	heat-stable entero

# SCORE Search Results Details for Application 10796719 and Search Result 20070326\_091528\_us-10-796-719a-31.rai.

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This page gives you Search Results detail for the Application 10796719 and Search Result 20070326\_091528\_us-10-796-719a-31.rai.

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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:02:53 ; Search time 53 Seconds  
(without alignments)  
23.121 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%
Query	

# SCORE Search Results Details for Application 10796719 and Search Result 20070326\_091531\_us-10-796-719a-31.rapbm.

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This page gives you Search Results detail for the Application 10796719 and Search Result 20070326\_091531\_us-10-796-719a-31.rapbm.

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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:03:06 ; Search time 185 Seconds  
(without alignments)  
35.054 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101

Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

# SCORE Search Results Details for Application 10796719 and Search Result 20070326\_091535\_us-10-796-719a-31.rapbn.

[Score Home Page](#)    [Retrieve Application List](#)    [SCORE System Overview](#)    [SCORE FAQ](#)    [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10796719 and Search Result 20070326\_091535\_us-10-796-719a-31.rapbn.

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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:04:21 ; Search time 89 Seconds  
(without alignments)  
32.021 Million cell updates/sec

Title: US-10-796-719A-31

Perfect score: 101

Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%